

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 9, 2002, 16:22:02 ; Search time 1762.53 Seconds
(without alignments)
2389.208 Million cell updates/sec

Title: US-09-880-887-9

Sequence: 1 gttgtttatgcacccctttt.....cgtatcttttaccattcag 312

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estcov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	47.2	15.1	734	12	CNS010MP
C 2	46.8	15.0	1101	12	CNS0039G
C 3	46.8	15.0	1101	12	CNS016L1
C 4	42.8	13.7	827	12	CNS00E03
5	42.6	13.7	1225	12	CNS0161D
6	42.4	13.6	948	12	CNS0159T
7	42	13.5	637	12	CNS036C
8	41.6	13.3	1101	12	CNS00H87
C 9	41	13.1	402	12	BT314726
C 10	41	13.1	979	12	CNS0161W
C 11	40.8	13.1	810	12	CNS010Y8
C 12	40.8	13.1	940	12	A2674355
C 13	40.6	13.0	483	9	BB247254
C 14	40.6	13.0	987	12	CNS014PO
C 15	40.4	12.9	524	12	CNS01U90
C 16	40.2	12.9	555	10	BT977182
17	40.2	12.9	987	12	CNS014PO

C 18	40	12.8	887	12	CNS00D5M	AL060256 Drosophill
C 19	40	12.8	1004	12	CNS00Bv2	AL058076 Drosophill
C 20	40	12.8	1101	12	CNS00262	AL097301 Drosophill
C 21	39.8	12.8	817	12	A2689592	A2689592 ENTHA57TR
C 22	39.8	12.8	856	12	A2680208	A2680208 ENTHA57TR
23	39.8	12.8	874	12	BH135257	BH135257 ENTHA57TR
24	39.8	12.8	896	12	CNS020G5	AL214430 Tetradodon
25	39.8	12.8	1101	12	CNS016TX	AL107199 Drosophill
26	39.6	12.7	495	12	AO192980	AO192980 HS_3053_A
C 27	39.4	12.6	915	12	CNS048RF	AL279636 Tetradodon
C 28	39.4	12.6	945	12	CNS04DOK	AL285149 Tetradodon
C 29	39.2	12.6	469	10	BM213762	BM213762 C0841C11-
C 30	39.2	12.6	675	12	A2974879	A2974879 C0841C11-
C 31	39.2	12.6	758	10	BS214880	BS214880 RST34535
32	39.2	12.6	1101	12	CNS00EFA	AL069119 Drosophill
33	39.2	12.6	1201	12	CNS0167M	AL106396 Drosophill
34	38.8	12.4	445	10	BE96412	BE96412 QV0-CT038
35	38.8	12.4	543	10	BM214243	BM214243 C0847H03-
36	38.8	12.4	548	10	BM216550	BM216550 C0882D04-
37	38.8	12.4	550	10	BM212068	BM212068 C0816F07-
38	38.8	12.4	578	10	BM214914	BM214914 C0857G10-
39	38.8	12.4	581	10	BM214098	BM214098 C0846B01-
40	38.8	12.4	646	10	BM213857	BM213857 C0842E11-
41	38.8	12.4	669	10	BM212059	BM212059 C0816E10-
C 42	38.8	12.4	683	9	AL514415	AL514415
C 43	38.8	12.4	898	12	A2543560	A2543560 ENTPD6OTR
C 44	38.6	12.4	695	12	AG043691	AG043691 Pan trogl
C 45	38.6	12.4	948	12	CNS0159T	AL105179 Drosophill

ALIGNMENTS

RESULT 1
CNS010MP/c
LOCUS
DEFINITION
CNS010MP
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN04L20 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION
AL099163
VERSION
AL099163.1 GI:5610774

KEYWORDS
GSS.

SOURCE
fruit fly.

ORGANISM
Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
1 (bases 1 to 734)

Genoscope.

Direct Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Recherche
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EGP) -
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC

library (DrosBAC) was made by Alain Billand at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC

project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector

pelobacil1.

Location/Qualifiers
1..734

source

FEATURES

source

/organism="Drosophila melanogaster"

/plasmid="pelobacil1"

/db_xref="taxon:7227"

/clone_lib="DrosBAC"

/clone="BACN04L20"

/note="end : T7"

BASE COUNT
288 a 62 c 2 g 211 t 171 others

ORIGIN

Query Match	15.0% ; Score 46.8 ; DB 12 ; Length 1101 ;
Best Local Similarity	25.9% ; Pred. No. 2.2 ;
Matches	76 ; Conservative 103 ; Mismatches 113 ; Indels 2 ; Gaps 1 ;
OY	18 ttttaaaatacatgtagatcgtccctttagatagaataatcgtatcgtctc 77
DB	721 DTRWDDAADDDTARDDRKRKGGDGDAGKGKTKGKRKRDRATWDRDAMDADAAWTT 662
OY	78 ttctaataatttgatcatatgattgacagaatatgaaagtcatacagccagcacg 137
DB	661 TDTDDDDMDKRDRKRKGGARRRRRTTARAAMDWMTWKAMDMKMDKTRDAMDADAAWTT 602
OY	138 caggtgtgaagtactgtygggaactcacagatttgctcctcagccctaaagaaatt 197
DB	601 TDARADRCMAAKARARARDRARARDRRTTKGTTTATWTTWAARAAMAWMAWTT 542
OY	198 ggccttcagatatttgatgattaaacaaagcttccttaagaagatgtaaatcttcacg 257
DB	541 TTAATTTTWTWTWTWTWTWTWTWTWTWTAAW--WMAAWMTATWMAWTAAMAAAAAAMA 484
OY	258 atgtttctcttttgcctaaactaaagaataacgcgatctctttacattca 311
DB	483 ATTTTTTTTTTTWTAAWMTAAWMTATWTTTWTWTWTWMAATTTTWTWTWMA 430
RESULT 3	
CNS016L1	
LOCUS	CNS016L1 1101 bp DNA linear GSS 26-JUL-1999
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC
KEYWORDS	BACN16D22 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL106896
VERSION	AL106896.1 GI:5624374
KEYWORDS	GSS.
SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster
REFERENCE	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
AUTHORS	Piercyota; Neoptera; Endopterygota; Diptera; Brachycera;
TITLE	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
JOURNAL	1 (bases 1 to 1101)
COMMENT	Genoscope. Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.
FEATURES	Location/Qualifiers
Source	1..1101
	/organism="Drosophila melanogaster"
	/plasmid="pBelobAC11"
	/db_xref="taxon:7227"
	/clone_lib="DrosBAC"
	/clone="BACN16D22"
	/note="end : T7"
BASE COUNT	203 a 220 c 84 g 158 t 436 others
ORIGIN	
Query Match	15.0% ; Score 46.8 ; DB 12 ; Length 1101 ;
Best Local Similarity	31.0% ; Pred. No. 2.2 ;
Matches	96 ; Conservative 69 ; Mismatches 145 ; Indels 0 ; Gaps 0 ;
OY	2 ttgtttatgcatcccttttaaatacatgagiatgctgcctttagatagaat 61

```

Db 790 TTTTNNATTTTNTTNDATNTTTTTTTTNTNTATATATTTTNTNTATATNTATNTAAATW 849
Qy 62 atctgagctgctctctcactaaatttgatcatgatttgacgaacatattgaag 121
Db 850 WTATTAATATATAMATAMATAMMTTAMMTDWTWMTTAKTWTATATATATATNTAW 909
Qy 122 tctaacgacccgacgcggttgtaagtaactgtygggaacttcacagatttgctcat 181
Db 910 AMWTAMAMAMATTTATTTWTWTTATTTATTTTATTTATTTTDTWTWNTARAAAMRWAT 969
Qy 182 gccctaaagaagaattggcttcagattcattgataaacaagaacttccttaag 241
Db 970 WMMAMAMATATMDTATNTATATATATATAAAMTMTWDTATTCGRMAMTADATTAMDAA 1029
Qy 242 atgtaaaattcattgattgcttcttcttctcctaaactaaagaattacgcgattctt 301
Db 1030 AATTAATATTTTWTWTTKTTTWTWTTTAKTAKAGRAMMTKAAARBMWRTTAD 1089
Qy 302 ttacattca 311
Db 1090 ATATATATATA 1099

```

```

RESULT 4
CNS00EU3 827 bp DNA linear GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC:
DEFINITION BACR29B23 of RPl-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL069854
VERSION AL069854.1 GI:4949806
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 827)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPl-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
p1 and Est libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridisation from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

```

```

FEATURES
source
1..827
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPl-98"
/clone="BACR29B23"
/note="end : TET3"
BASE COUNT 181 a 107 c 46 g 163 t 330 others
ORIGIN

```

```

Query Match 13.7%; Score 42.8; DB 12; Length 827;
Best Local Similarity 20.2%; Pred. No. 16;
Matches 55; Conservative 109; Mismatches 108; Indels 0; Gaps 0;

```

```

Qy 39 gcttcgctttagatatagaatatcgtctcttcactaaatttgattacat 98
Db 790 GMKRBRDRAKMTKMDYAAKGRTGVRKKWGTXTTKTRHKRVGTAISATYAAT 731
Qy 99 gattgacacaatatgaaagacttcaacgacgacgacgaggttgtaagtaactgtgag 158
Db 730 AATYMMHVMATTAATAMMMMMWMTATRKVKRRDADRDTGDMKTRCKDPTAATSAG 671
Qy 159 aacatcacagatttgctccatgcctaaagaagaattgcttcagattattgatt 218
Db 670 AGDYABAKATVTTWNTTWTWNRRTTKWTTTAAAMRAKADADARAAMWMTWHRM 611
Qy 219 aaaaacaagacttcttaagagatgaaatttcattgattgcttccttgcctaa 278
Db 610 NRATVAMMTATWMDAADAAHAAHAKATWADHAAWMTAMKVKWVGDTTWRKYSKM 551
Qy 279 ctaagaattacgcgattcattcattc 310
Db 550 HHCMNTAMATAMAAAGHDTADHWTYTMAYHTWV 519

```

```

RESULT 5
CNS0161D 1225 bp DNA linear GSS 26-JUL-1999
LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION BACN15C18 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL106171
VERSION AL106171.1 GI:5620504
KEYWORDS GSS.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1225)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (BDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billand at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pbeloBAC11.

```

```

FEATURES
source
1..1225
/organism="Drosophila melanogaster"
/plasmid="pbeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN15C18"
/note="end : SP6"
BASE COUNT 266 a 128 c 38 g 368 t 425 others
ORIGIN

```

```

Query Match 13.7%; Score 42.6; DB 12; Length 1225;
Best Local Similarity 35.3%; Pred. No. 17;
Matches 76; Conservative 42; Mismatches 101; Indels 0; Gaps 0;
Qy 50 agatatagaatatcgtctcttctcactaaatttgattacatgattgacagc 109
Db 887 AAAAAAAMMMWMTTYYTAYAAVAAVAMATMTTATAAAMWAAAAAAM 946
Qy 110 aatattgaagatcacaacgacgacgaggttgtaagtaactgtygggaacatcacaga 169
Db 947 AMWTTTAAAAAAMTAAATATATTTTATTTTAAWMTTATATTAATTTATTT 1006

```

OY	170	ctttgctccacgcacctaaagaagatcgcttccaatatatttgatgaataacaaga	229
Dd	1007	: : : : : : : : :	1066
OY	230	cttcttaagaagatgtaaaatttcocatgatgtcttctttt 270	
Dd	1067	: : : : : : : : : : yTTTTATATTMMAMAWMTWTWTWTWTWTWTWTWTWT 1107	
RESULT	6		
CNS0159T			
LOCUS	CNS0159T	948 bp	DNA linear GSS 26-JUL-1999
DEFINITION	Drosophila melanogaster genome survey sequence T7 end of BAC BACN13A12 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.		
ACCESSION	AL105179	GI:5617193	
VERSION	ALI05179.1		
KEYWORDS	GSS,		
SOURCE	fruit fly,		
ORGANISM	Drosophila melanogaster		
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 948)		
REFERENCE	Genoscope, Direct Submision Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage ; : : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (BDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.		
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source	Location/Qualifiers		
	1..948		
	/organism="Drosophila melanogaster"		
	/plasmid="pBelobAC11"		
	/db_xref="taxon:7227"		
	/clone_1lb="DrosBAC"		
	/clone="BACN13A12"		
	/note="end : 77"		
BASE COUNT	110 a 73 c 109 g 297 t 359 others		
ORIGIN			
Query Match	13.6%;	Score 42.4;	DB 12; Length 948;
Best Local Similarity	20.6%;	Pred. No. 19;	
Matches	48; Conservative	91; Mismatches	94; Indels 0; Gaps 0;
OY	74	cttctcaactaatatttatcatcagatttgcacgaatatgtgaagagtctaacagcaag	133
Dd	635	MTTTMMNTHTMMNMHTTTTKGMYAGMGTIVNGOMMMKMKMGVNNMGGMMM 694	
OY	134	caacgagatgttgtaagtcctgtggacaacacagatlttgctccatgcctsaagaga	193
Dd	695	VKGKMGKMGKMKKKMKKKMGVYKGVVMKCMKMKKKMKMKMKMKMKMKMK 754	
OY	194	aattgcttcagatatttgtatgtatgaataaacagactctttaagagatgaaattt	253
Dd	755	KMTKKKKKKKKKKAKKAKKKAAAAAAKAKKAKKAKKAKKAKKADAAWTTTTTAAAT	814
OY	254	catagtgttcttcttcttgctaaacataagaatgaocgvtatcttttaca	306
Dd	815	TWTAAATAATWTTTWTWMTTAAMWKTAVMAWMTWTTAWMATKAKATAADA	867
RESULT	7		
CNS036CC			
LOCUS	CNS036CC	637 bp	DNA linear GSS 15-MAY-2000

DEFINITION	Tetradon nigroviridis genome survey sequence PUC-Ort end of clone 215L21 of library G from Tetradon nigroviridis, genomic survey sequence.
ACCESSION	AL229845
VERSION	AL229845.1 GI:7888840
KEYWORDS	GSS: genome survey sequence.
SOURCE	Tetradon nigroviridis.
ORGANISM	Tetradon nigroviridis.
REFERENCE	Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodonidae; Tetradon.
AUTHORS	1 (bases 1 to 637) Roest-Crollius,H., Jallion,O., Dasilva,C., Fizesac,C., Fisher,C., Bouneau,L., Billault,A., Queller,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigroviridis Unpublished
JOURNAL	2 (bases 1 to 637)
REFERENCE	Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizesac,C., Wincker,P., Brottier,P., Queller,F., Saurin,W. and Weissenbach,J. Human gene number estimate provided by genome wide analysis using Tetradon nigroviridis DNA sequence Unpublished
TITLE	3 (bases 1 to 637) Genoscope.
JOURNAL	Direct Submission
AUTHORS	Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT	This sequence is a single read and was generated as part of a large scale clone-and-sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetradon .
FEATURES	Location/Qualifiers 1..637 /organism="Tetradon nigroviridis" /db_xref="taxon:99883" /cloae="215L21" /clone_1ib="G" /note="Genoscope sequence ID : C0AG215CF11SP1-end : PUC-Ort"
BASE COUNT	180 a 95 c 80 g 224 t 58 others
ORIGIN	
Query Match	13.5%; Score 42; DB 12; Length 637;
Best Local Similarity	38.0%; Pred. No. 24;
Matches 117; Conservative 33; Mismatches 158; Indels 0; Gaps 0;	
OY 2 ttgttatgatccctttttaaatatcatgaglatgctgccttttagatatagaat 61	:::: :: :: :: :: :
Db 308 TTTTGTTTTTTTTTTTTWWAAAAAAMWMAAMCMMWAAAWTTTTTTTTTTTWWAAAAAAM 367	
OY 62 atcgaigcigtcttcctactaaatttgattcatgattggcagcaatatgaag 121	
Db 368 TTTTWTWWTTTTTTTTTWWAAAAAAMWMAAMCMMWAAAWTTTTTTTTTTTWWAAAAAAM 427	
OY 122 tctaaccgccagcgacgagcttglaagtactgigggaacctcacagatttggctcat 181	::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 428 WATTAATAAAAAAAAAAAWMTTWTWTAATAAAAAAAAAAAWMAAMWMTTWMAAAAAA 487	
OY 182 gccctaaagagaattggcttcagatatattgatttaaacacaagactctctaag 241	: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 488 AMTTTTTTTTTTTAAAAAAAAMWTTTTTTTTTTTWWAAAAAAMWTAAMWTTTTTWMWA 547	
OY 242 atgtaaatctcagatgattctctcttcctaataaagaagattaacgcatctc 301	:: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 548 AMAAAAMWTTTTTTTTTTTWTWMTWTTTTTTTATTTTTTTAAAAAAMWAAAAAATTTT 607	
OY 302 ttacatt 309	: :
Db 608 TTWTTTTTT 615	

```

RESULT      8
CNS00H87    1101 bp  DNA  linear  GSS 03-JUN-1999
LOCUS
DEFINITION   Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR34J09 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION    AL073055.1  GI:4952936
VERSION      AL073055.1  GI:4952936
KEYWORDS     GSS.
SOURCE       fruit fly.
ORGANISM     Drosophila melanogaster
              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
              Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
              Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE    1 (bases 1 to 1101)
AUTHORS      Genoscope.
TITLE        Direct Submission
JOURNAL      Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT      Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see: http://www.fruitfly.org/the_BDGP_Drosophila
melanogaster_BAC_library.html
              melanogaster BAC library was prepared by Kazutoyo Osogawa and
              Aaron Mammoser in Pieter de Jong's laboratory in the Department of
              Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
              NY. The library is named RPCI-98 and was constructed by partial
              EcoRI digestion of Drosophila DNA provided by the BDGP from the
              isogenic strain y2; cn bw sp, the same strain used for the BDGP's
              pl and EST libraries. A more detailed description of the library
              and how to order individual BAC clones, the entire library, or
              filters for hybridization from the BACPAC Resource Center can be
              found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
    source
        1..1101
            /organism="Drosophila melanogaster"
            /db_xref="taxon:7227"
            /clone_lib="RPCI-98"
            /clone="BACR34J09"
            /note="end="TET3"

BASE COUNT   149 a      86 c      62 g      380 t      424 others
ORIGIN
Query Match      13.3%; Score 41.6; DB 12; Length 1101;
Best Local Similarity 34.8%; Pred. No. 28;
Matches 104; Conservative 1; Mismatches 194; Indels 0; Gaps 0;

OY  2 ttgtttatcatcctttttaaatatcatgagtgatgcttcgtcctttagatagaat 61
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  91 TTTTNTNTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAAAT 150
OY  62 atgcagtcgctctctcctaatttgatcatgattgacagcaatatgaag 121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  151 ATCTTAATTAATCCTTNTNTTTTTTTTTTTTTTTTTTTTTTTTAAATTTANNNAN 210
OY  122 tctaacgacgacgagcttgtaagctgtaagctggaacatcacagattggtccat 181
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  211 NNANNNNNNNNNNTTATTTTTTTTTTTTTTTNNNNNNNTTATTTTATTTATNT 270
OY  182 gccctaaaggaattggtcttcagattatctgattaaacaagaacttcctaag 241
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  271 AANNNNNNNNNAATAATTTANNNANNNANNAATTAATTTTATTAANN 330
OY  242 atgcaaatcttcagtgtttcttttgcctaaactaaagaatgaagcgatctct 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  331 ANNNNNNAANNNTTNTTTTTTATTTTTTTTAAATANANAAAAAANNNNTTAAANT 389

```

```

RESULT      9
BI314726/c  402 bp  mRNA  linear  EST 20-JUL-2001
LOCUS
DEFINITION   BI314726 dae53f11.y1 Blackshear/Soares normalized Xenopus egg library
Xenopus laevis cDNA clone IMAGE:4678028 5', mRNA sequence.
ACCESSION    BI314726
VERSION      BI314726.1  GI:14989053
KEYWORDS     EST.
SOURCE       African clawed frog.
ORGANISM     Xenopus laevis
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
              Xenopodinae; Xenopus.
REFERENCE    1 (bases 1 to 402)
AUTHORS      Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Page,D.,
              Martin,J., Wylie,T., Underwood,K., Treising,B., Bowers,Y., Person
              'B.', Gibbons,M., Harvey,N., Rilter,E., Jackson,Y., McCann,R.,
              Waterston,R. and Wilson,R.
              Washu Xenopus EST project, 1999
              Unpublished (1999)
              Contact: Sandy Clifton, Ph.D.
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              Library constructed by Bento Soares and M. Fatima Bonaldo
              (University of Iowa). DNA Sequencing by: Washington University
              Genome Sequencing Center
              Clone distribution: Xenopus clones from this library are available
              through the I.M.A.G.E. Consortium/LINL at: info@image.llnl.gov
              Seq primer: -40BP from Glpco
              High quality sequence stop: 371.

FEATURES
    source
        1..402
            /organism="Xenopus laevis"
            /db_xref="taxon:8355"
            /clone="IMAGE:4678028"
            /clone_lib="Blackshear/Soares normalized Xenopus egg
            library"
            /sex="female"
            /tissue_type="unfertilized egg"
            /cell_type="unfertilized egg"
            /dev_stage="unfertilized egg"
            /lab_host="DH10B"
            /note="Vector: pT7T3-Pac; Site.1: EcoRI; Site.2: NotI.
            Polya-selected mRNA was prepared from unfertilized Xenopus
            laevis eggs. The library was constructed in the vector
            pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and
            Soares, M.B. 'Normalization and subtraction: two
            approaches to facilitate gene discovery', Genome Research
            6:791-806, 1996. The first strand synthesis used a
            NotI-dT18 primer; double stranded cDNAs were ligated to
            EcoRI adapters, digested with NotI, and directionally
            cloned into the NotI and EcoRI-digested pT7T3-Pac vector.
            The library contained approximately 7.2 x 105
            recombinants, with average insert sizes of 1-1.5 kb."

BASE COUNT   137 a      49 c      46 g      170 t
ORIGIN
Query Match      13.1%; Score 41; DB 10; Length 402;
Best Local Similarity 47.8%; Pred. No. 42;
Matches 119; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

OY  14 tcccttttaaatcatgagatgctgctctttagatataagaatatcgtgctgt 73
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  393 TCATTTTAAATGCTATATATATATATATATATATATATATATATATATATATAT 334
OY  74 ctctctactaaatttgattcatgatgattgacgacaaatatgaagagctcaacg 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  333 ATATATATATATATATATATATATATATATATATATATATATATATATATAT 274

```

Qy	258	atgcttcttcttgcctaaactaaagaactaaacgcgtatcttacc 306
		1: : : : : : : :
Db	663	ANATTMTMTAKAKAGWTTAAAAAGAMMADKMTATGAGAAAMTTTMAA 615
RESULT	11	
LOCUS	CNS010Y8/C	
DEFINITION	CNS010Y8	810 bp DNA linear GSS 26-JUL-1999
ACCESSION	Drosophila melanogaster genome survey sequence SP6 end of BAC	
VERSION	BAC005022 of DrosBAC library from Drosophila melanogaster (fruit	
KEYWORDS	fly), genomic survey sequence.	
SOURCE	AL099578.1 GI:5611189	
ORGANISM	GSS.	
	fruit fly.	
	Drosophila melanogaster	
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;	
	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
REFERENCE	1 (bases 1 to 810)	
AUTHORS	Genoscope.	
TITLE	Direct Submission	
JOURNAL	Submitted (23-JUN-1999) Genoscope - Centre National de Sequence : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (PDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CPBH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.	
FEATURES		
source	Location/Qualifiers	
	1..810	
	/organism="Drosophila melanogaster"	
	/plasmid="pBelobAC11"	
	/db_xref="taxon:7227"	
	/clone_11b="DrosBAC"	
	/clone="BACN05D22"	
	/note="end : SP6"	
BASE COUNT	247 a 138 c 168 g 170 t 87 others	
ORIGIN		
Query Match	13.1%; Score 40.8; DB 12; Length 810;	
Best Local Similarity	52.0%; Pred. No. 43;	
Matches	51; Conservative 12; Mismatches 35; Indels 0; Gaps 0;	
Qy	177	tccatgccttaagaagaatggccttcataagattatcgtgataaacaagaacttctt 236
	: :: : :	
Db	108	TCCATTCCTCCCTCKKYAATTTGGCCCTTCACCKHMYAACCAHHAMADGCANMGCGGTCGG 49
Qy	237	aagaatgtaaatattcatgatgttcttcttcttgc 274
Db	48	ANGAANAAGAGCAANTTTATNATNTTTTCTTTTWT 11
RESULT	12	
LOCUS	A2674355	940 bp DNA linear GSS 14-DEC-2000
DEFINITION	ENT1164TR Entamoeba histolytica Sheared DNA Entamoeba histolytica	
ACCESSION	genomic, DNA sequence.	
VERSION	A2674355	
KEYWORDS	A2674355.1 GI:11811501	
SOURCE	GSS.	
ORGANISM	Entamoeba histolytica.	
	Entamoeba histolytica	
	Eukaryota; Entamoebidae; Entamoeba.	
REFERENCE	1 (bases 1 to 940)	
AUTHORS	Loftus,B., Van Aken,S. and Fraser,C.	
TITLE	Determination of clone and sequences from Entamoeba histolytica	

Db 113 WWWWWWWWWWWWWWWWWWWWWTTTTTTTTTATWTTATTTTTTTTTTTW 172
Qy 268 ttTgCtaactaaagaat 287
||| ||| ||| |||
Db 173 TTTTTTAAATTAATAATAT 192

Search completed: September 9, 2002, 20:42:51
Job time: 15649 sec

